

Fig. 2

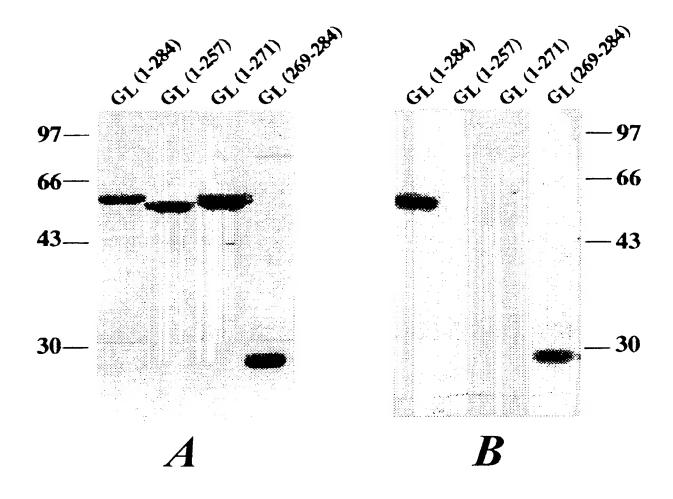
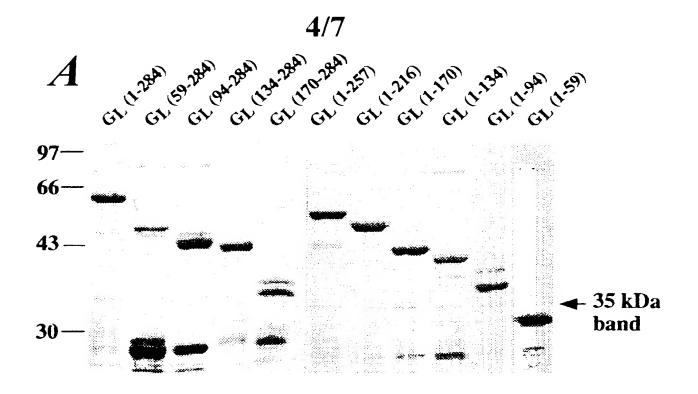


Fig. 3



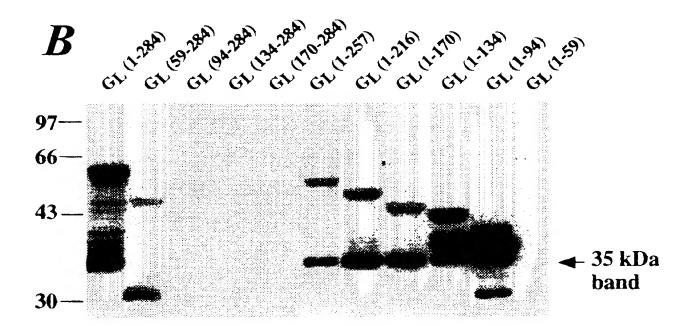


Fig. 4

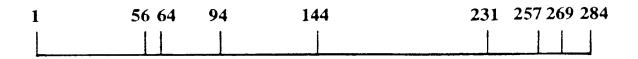
SUBSTITUTE SHEET (RULE 26)

M ₁₁₀ (1-38) peptide	26	PPVV <u>KRQK</u> T <u>KVKF</u>	38
${ t G}_{ t L}$	52	TVQE <u>KK</u> V <u>K</u> KRVSFADQGL	69
G _M (63-93) peptide	63	GRRVSFADNFG	73

Fig. 5

$G_{ m L}$	132	VCLENCVLKEKALAGTVKVQNLAFEKVVKIRMTFDTWKSFT	172
R5	157	VCLENCSLQERTYTGTYKYKNYSFEKKYOLRITFDSWKNYT	197
R6	177	VCLERVTCSDLGLSGTVRVCNVAFEKOVAVRYTFSGWRSTH	217
G_{M}	128	Alles-tesligstsikgiirvlmvsfekuvyvrmslddmothy	170
GAC1	244	VKLHSLTQLGDDSSKLTGLVYVKNLSFEKYLEIKETFNSWRDIH	287
AMYL Conse	33 ens u s	VQLDSYNYDGSTFSGKIYVKNIAYSKKVTVIYADGSDNWNNNG \$\oplus \cdot \overline{\text{U}} \cdot \overline{\text{V}} \overline{\text{V}} \cdot \overline{\text{V}} \overline{\text{V}} \cdot \overline{\text{V}} \cdot \overline{\text{V}} \overline{\text{V}} \overline{\text{V}} \cdot \overline{\text{V}} \overlin	75
PHOS	398	RHLQI <u>IYEIMQRFLNRV</u> AAA <u>F</u> PGDVDRLRRMS	429
		** ***	
${ t G}_{ t L}$	173	DFPCQYVKDTYAGSDRDTFSFDISLPEKIQSYE	205
R5	19 8	DVDCVYMKNVYGGTDSDTESEAIDLPPVIPTEQ	230
R6	218	EAVARWRGPAGPEGTEDVFTFGFPVPPFLLELGS	251
G_{M}	171	DILAEYVPNSCDG-ETDOESEKIVLVPPYQKDGS	203
GAC1	288	YVTANFNRTINSNVDEFKFTIDLNSLKYILLIKRIITMEKNTSS	3 31
	76	NTIAASYSAPISGSNYEYWTESASINGIK	104
Conse	ensus	D.F. F φ Ε W	
PHOS	330	LVEEGAVK	437
FHOS	330	* * *	437
$G_{T_{i}}$	206	RMEFAVCYECNGQSYWDSNKGKNYRI	231
R5	231	KIEFCISYHANGQVFWDNNDGQNYRI	256
R6	252	RVHFAVRYQVAGAEYWDNNDHRDYSL	282
G_{M}	204	KVEFCIRYETSVGTFWSNNNGTNYTF	229
GAC1	332	CPLNIELCCRYDVNNETYYDNNNGKNYHL	360
AMYL	_	EFYIKYEVSGKTYYDNNNSANYQV	128
Conse	ensus	$\mathbf{F}. \mathbf{\phi}. \overline{\mathbf{Y}}. \ldots \mathbf{YW}. \overline{\mathbf{N}}. \ldots \overline{\mathbf{Y}}. \mathbf{\phi}$	

Fig. 6



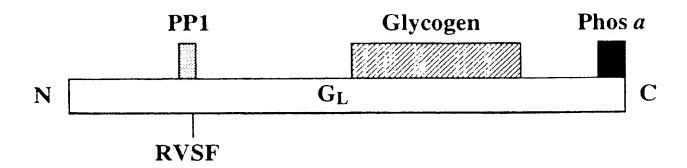


Fig. 7